



PATENT
ATTORNEY DOCKET NO.: 00786/246002

#20
10/11/02

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Christine M. Citro

Signature of person mailing correspondence

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant: David Moore et al.

Art Unit: 1646

Serial No.: 09/365,576

Examiner: M. Pak

Filed: August 2, 1999

Customer No.: 21559

Title: RETINOID X RECEPTOR-INTERACTING POLYPEPTIDES AND
RELATED MOLECULES AND METHODS

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Commissioner for Patents
Washington, D.C. 20231

DECLARATION OF DR. DAVID MOORE UNDER 37 C.F.R. § 1.131

I, David Moore, declare that:

1. I am an inventor of the invention described and claimed in the
above-identified patent application.

2. The present claims of the application recite retinoid X receptor-interacting proteins
that have an amino acid sequence at least 85% identical to that of RIP15.

3. The other inventors and I conceived of, and reduced to practice, the claimed subject
matter of the present application prior to November 10, 1993.

4. The reduction to practice of the claimed invention is evidenced by Exhibit 1 annexed hereto. The date of Exhibit 1 has been redacted in accordance with the standard practice, but is prior to November 10, 1993. Exhibit 1 contains the entire amino acid sequence of RIP15, which was predicted based on the sequence of a full-length RIP15 cDNA. The isolation of the RIP15 cDNA was performed by Wongi Seol, another inventor of the claimed invention. The isolation and sequencing of the RIP15 cDNA was carried out in the United States prior to November 10, 1993.

5. As described in the present application and in the Declaration filed December 28, 2001, a RIP15 clone was isolated in an *in vivo* interaction trap assay designed to isolate cDNA molecules encoding proteins that interact with the retinoid X receptor (RXR). For this assay, a mouse cDNA library was introduced into yeast that expressed a LexA-RXR fusion protein and that contained β -galactosidase and LEU2 genes under the control of LexA binding sites. LexA-RXR is not a strong transcriptional activator in yeast. However, LexA-RXR activates expression from LexA binding sites in cells which also express a fusion protein consisting of a transcriptional activation domain joined to another protein which interacts specifically with RXR (as described on pages 12 and 25-27 of the specification).

Clone 15 which encodes RIP15 was isolated in this assay based on its ability to induce expression of both β -galactosidase and LEU2, indicating that it encoded a protein that interacted with RXR.

6. The plasmid was isolated from selected yeast clone 15 and transferred into

E. coli for analysis. In particular, the plasmid was purified from *E. coli* and digested with restriction enzymes to determine the size of the cDNA insert in the plasmid. Based on the migration of the restriction enzyme-digested cleavage product in the agarose gel, the cDNA insert was determined to be approximately 4.0 kDa. A region from this cDNA insert was used as a hybridization probe to isolate the full-length RIP15 coding sequence from a mouse cDNA library, as described on page 27 of the specification.

7. This full-length RIP15 cDNA was sequenced prior to November 10, 1993. Exhibit 1 contains the full-length translated amino acid sequence of RIP15.

8. I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patents issued thereon.

Date: 10/23/02



David Moore, Ph.D.
Professor
Molecular & Cellular Biology
Baylor College of Medicine

Exhibit 1

\$ dir rxr*

Directory MOORE_LAB:[MOORE]

RXR14.;1	RXR14D.OUT;1	RXR14E.;2
RXR14E.OUT;3		
RXR15.;2	RXR15E.;2	RXR15E.OUT;2
RXRG.;2		

Total of 8 files.

\$ ty rxr15.

rxr interacting clone 15 full length

Rxr15. Length: 446	Type: P	Check:
7438 ..		

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1  MSSPTSSLDT PVPNGNGSPQP STSATSPTIK EEGQETDPPP GSEGSSSAYI
51  VVILEPEDEP ERKRKKGPAP KMLGHELCRV CGDKASGFHY NVLSCEGCKG
101 FFRRSVVHGG AGRYACRGSG TCQMDAFMRR KCQLCRLRKC KEAGMREQCV
151 LSEEQIRKKR IQKQQQQQPP PPSEPAASSS GRPAASPGTS EASSQGSgeg
201 EGIQLTAAQE LMIQQLVAAQ LQCNKRSFSD QPKVTPWPLG ADPQSRDARQ
251 QRFAHFTELA IISVQEIVDF AKQVPGFLQL GREDQIALLK ASTIEIMLLE
301 TARRYNHETE CITFLKDFTY SKDDFHRAGL QVEFINPIFE FSRAMRRLGL
351 DDAEYALLIA INIFSADRPN VQEPSRVEAL QQPYVEALLS YTRIKRPQDH
401 VRFPRMLMKL VSLRTLSSVH SEQVFALRLQ DKKLPPLLSE IWDVHE
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